

Abstract of Poster Presentation

Genetic diversity of *Xanthomonas* species pathogenic to citrus based on *avr* and *leucine rich protein* genes

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The genus *Xanthomonas* includes a group of phytopathogenic bacteria that have great economic importance around the world. Citrus canker, caused by *Xanthomonas citri* subsp. *citri*, is one of the main threats to citrus crops worldwide. Different forms of citrus canker have been described based on pathogen specificity and geographical origin, and are caused by other two *Xanthomonas* species: *X. alfalfae* subsp. *citrumelonis* and *X. fuscans* subsp. *aurantifolii*. In the present work we developed DNA primers and probes based on pathogenicity genes in order to study the genetic diversity of these three *Xanthomonas* species, specially a Brazilian population of *citri* strains. The presence of *avrXacE1*, *avrXacE2*, *avrXacE3* and *leucine rich protein (lrp)* genes were observed in almost all *citri* and *aurantifolii* strains, but *avrXacE2* and *avrXacE3* genes were absent in *citrumelonis* strains. The profiles generated by PCR-RFLP of the *avr* genes did not display any polymorphism after agarose gel electrophoresis. However the use of *avr* genes as Southern blot probes proved to be effective to differentiate *Xanthomonas* species pathogenic on citrus and to identify polymorphisms between strains belonging to the same species from Brazil. With the exception of the probe corresponding to *lrp* gene, the number of haplotypes identified (22) varied according to the gene/endonuclease used on Southern blot. The strains of subspecies *citri* possess a higher number of copies of the *avr* genes than subspecies *aurantifolii* and *citrumelonis*. Relatively high genetic diversity was observed in *citri* and *aurantifolii* Brazilian populations, independently of the citrus canker control method applied in the area of origin of the strains.